

[illegible]

<120> Groups of *Borrelia burgdorferi* and  
*Borrelia afzelii* That Cause Lyme Disease in Humans

<150> US 60/140,042  
<151> 1999-06-18

<170> FastSEQ for Windows Version 4.0

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<220>  
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<210> 5  
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser 15  
1 5 10

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 30  
20 25

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 45  
35 40

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 60  
50 55

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 80  
65 70 75

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 95  
85 90

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys 110  
100 105

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 125  
115 120

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 140  
130 135

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 160  
145 150 155

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 175  
165 170

Sub A1

0056745-061900

3/102

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 175  
165 170

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat gga tcc 573  
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180 185

<210> 6  
<211> 190  
<212> PRT  
<213> borrelia burgdorferi

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20 25  
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu 45  
35 40  
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys 60  
50 55  
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu 80  
65 70 75  
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys 95  
85 90  
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys 110  
100 105  
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu 125  
115 120  
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys 140  
130 135  
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu 160  
145 150 155  
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 175  
165 170  
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Ser 190  
180 185

<210> 7  
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<212> DNA  
<213> Borrelia burgdorferi

<220>  
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<222> (1)...(557)

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1 5 10

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 30  
20 25

0050715-05100

Sub A1

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 35 40 45  
 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 50 55 60  
 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
 65 70 75 80  
 tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
 85 90 95  
 gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
 100 105 110  
 tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
 115 120 125  
 ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
 130 135 140  
 aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
 145 150 155 160  
 aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
 165 170 175  
 gct gtt aaa gag ctt aca agt cct att gt 557  
 Ala Val Lys Glu Leu Thr Ser Pro Ile  
 180 185

<210> 8  
 <211> 184  
 <212> PRT  
 <213> Borrelia burgdorferi

<400> 8  
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 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu  
 35 40 45  
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile  
 50 55 60  
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu  
 65 70 75 80  
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val  
 85 90 95

00506716-05100

SubA1

Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys  
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 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly  
 115 120 125  
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys  
 130 135 140  
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys  
 145 150 155 160  
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala  
 165 170 175  
 Val Lys Glu Leu Thr Ser Pro Ile  
 180

<210> 9  
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 <212> DNA  
 <213> Borrelia burgdorferi

<220>  
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 1 5 10 15  
 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
 20 25 30  
 aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144  
 Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala  
 35 40 45  
 gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192  
 Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Ile Ala Ala  
 50 55 60  
 aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat acc gaa 240  
 Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu  
 65 70 75 80  
 aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288  
 Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr  
 85 90 95  
 cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336  
 Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu  
 100 105 110  
 aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384  
 Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu  
 115 120 125  
 aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat 432  
 Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp  
 130 135 140

005715-000

Sub A1

Sub A1

gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa ggt gct	480
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145 150 155 160	
gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca	528
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt	576
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val	
180 185 190	
gtg	579
Val	

<210> 10  
 <211> 192  
 <212> PRT  
 <213> Borrelia burgdorferi

<400> 10

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Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val	
35 40 45	
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn	
65 70 75 80	
Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu	
85 90 95	
Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys	
100 105 110	
Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys	
115 120 125	
Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala	
130 135 140	
Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu	
145 150 155 160	
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165 170 175	
Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val	
180 185 190	

<210> 11  
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 <212> DNA  
 <213> Borrelia brgdorferi

<220>  
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006750-949550

**SECRET**

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SubA1

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 Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val  
 35 40 45  
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala  
 50 55 60  
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn  
 65 70 75 80  
 Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile  
 85 90 95  
 Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys  
 100 105 110  
 Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys  
 115 120 125  
 Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala  
 130 135 140  
 Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val  
 145 150 155 160  
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 165 170 175  
 Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val  
 180 185 190  
 Val

<210> 13  
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 <213> Borrelia burgdorferi

<220>  
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 1 5 10 15  
 aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
 Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
 20 25 30  
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144  
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
 35 40 45  
 gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192  
 Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
 50 55 60  
 aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag 240  
 Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
 65 70 75 80

agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288  
 Ser Lys Asn Thr Ser 85 Gly Ala Tyr Ala Ile Ser Asp Leu 95  
 ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336  
 Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys 110  
 att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384  
 Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys 125  
 agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432  
 Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala 140  
 caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480  
 Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala 160  
 gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528  
 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala 175  
 caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576  
 Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val 190

<210> 14  
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 Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val  
 35 40 45  
 Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys  
 50 55 60  
 Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser  
 65 70 75 80  
 Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile  
 85 90 95  
 Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile  
 100 105 110  
 Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser  
 115 120 125  
 Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln  
 130 135 140  
 Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu  
 145 150 155 160  
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln  
 165 170 175

00556746-051900

Sub A1

Sub-A1  
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 180 185 190

<210> 15  
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 <212> DNA  
 <213> borrelia burgdorferi

<220>  
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 1 5 10 15  
 aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt 96  
 Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
 20 25 30  
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144  
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
 35 40 45  
 gtg aaa gaa gtt gag acc tta ttt gca tct ata gat gaa ctt gct acc 192  
 Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
 50 55 60  
 aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag 240  
 Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln  
 65 70 75 80  
 agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288  
 Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu  
 85 90 95  
 ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336  
 Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys  
 100 105 110  
 att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384  
 Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys  
 115 120 125  
 agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432  
 Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala  
 130 135 140  
 caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480  
 Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala  
 145 150 155 160  
 gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528  
 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala  
 165 170 175

006146-061900

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576  
 Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
 180 185 190

<210> 16  
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 <212> PRT  
 <213> borrelia burgdorferi

<400> 16  
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 Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val  
 35 40 45  
 Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys  
 50 55 60  
 Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser  
 65 70 75 80  
 Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile  
 85 90 95  
 Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile  
 100 105 110  
 Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser  
 115 120 125  
 Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln  
 130 135 140  
 Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu  
 145 150 155 160  
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 Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val  
 180 185 190

<210> 17  
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<220>  
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<400> 17  
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 1 5 10 15  
 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
 20 25 30  
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc 144  
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
 35 40 45

005190-949560

Sub A1

gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa 192  
 Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys  
 50 55 60  
 gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca 240  
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala  
 65 70 75 80  
 gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta 288  
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu  
 85 90 95  
 ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca 336  
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala  
 100 105 110  
 gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta 384  
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu  
 115 120 125  
 aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat 432  
 Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn  
 130 135 140  
 gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct 480  
 Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala  
 145 150 155 160  
 gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca 528  
 Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala  
 165 170 175  
 gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct 573  
 Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro  
 180 185 190

<210> 18  
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 <212> PRT  
 <213> Borrelia burgdorferi

<400> 18  
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 20 25 30  
 Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val  
 35 40 45  
 Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala  
 50 55 60  
 Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp  
 65 70 75 80  
 His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile  
 85 90 95  
 Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu  
 100 105 110

00596745-051900

Sub A1

Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys  
 115 120 125  
 Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala  
 130 135 140  
 Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp  
 145 150 155 160  
 Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala  
 165 170 175  
 Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro  
 180 185 190

<210> 19  
 <211> 553  
 <212> DNA  
 <213> *Borrelia burgdorferi*

<220>  
 <221> CDS  
 <222> (1)...(553)

<400> 19  
 atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48  
 Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly  
 1 5 10 15  
 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96  
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
 20 25 30  
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144  
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
 35 40 45  
 gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192  
 Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr  
 50 55 60  
 aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa 240  
 Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu  
 65 70 75 80  
 gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act 288  
 Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr  
 85 90 95  
 gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa 336  
 Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys  
 100 105 110  
 gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa 384  
 Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys  
 115 120 125  
 tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat 432  
 Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp  
 130 135 140



**THE UNIVERSITY OF CHICAGO**

~~<400> 22  
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn  
1 5 10 15  
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr  
20 25 30~~

**SECRET**

<220>  
<223> OspC Chimera

<400> 23																
atg	gct	tgt	aat	aat	tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	48
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	
1				5					10					15		
<hr/>																
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	96
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
			20					25					30			
<hr/>																
att	acg	gat	tct	aat	gcg	gtt	tta	ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	144
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	
		35					40					45				
<hr/>																
ttg	ctg	tca	tct	ata	gat	gaa	att	gct	gct	aaa	gct	att	ggg	aaa	aaa	192
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	
	50					55				60						
<hr/>																
ata	cac	caa	aat	aat	ggg	ttg	gat	acc	gaa	tat	aat	cac	aat	gga	tca	240
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	
65					70					75					80	

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
 85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
 100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
 180 185 190

atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct 624  
 Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
 195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
 210 215 220

aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg 720  
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu  
 225 230 235 240

ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa 768  
 Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys  
 245 250 255

aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata 816  
 Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile  
 260 265 270

tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca 864  
 Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala  
 275 280 285

ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa 912  
 Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys  
 290 295 300

tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt 960  
 Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu  
 305 310 315 320

00596745-051900

Sub-A1

Sub A1

ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa 1008  
 Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
 325 330 335

aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt 1056  
 Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe  
 340 345 350

gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat 1104  
 Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn  
 355 360 365

tca gtt aaa gag ctt aca agc taa 1128  
 Ser Val Lys Glu Leu Thr Ser \*  
 370 375

<210> 24  
 <211> 374  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 24  
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
 1 5 10 15  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
 20 25 30  
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu  
 35 40 45  
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60  
 His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu  
 65 70 75 80  
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp  
 85 90 95  
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys  
 100 105 110  
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu  
 115 120 125  
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys  
 130 135 140  
 Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe  
 145 150 155 160  
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn  
 165 170 175  
 Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met  
 180 185 190  
 Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp  
 195 200 205  
 Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr  
 210 215 220  
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu  
 225 230 235 240  
 Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn  
 245 250 255

00612909436560

19/102

Sub A1

Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser 270  
 Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile 285  
 Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys 300  
 Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly 320  
 Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr 335  
 Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu 350  
 Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser 365  
 Val Lys Glu Leu Thr Ser 370

<210> 25  
 <211> 1124  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OSpC Chimera

<221> CDS  
 <222> (1)...(1124)

<400> 25  
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser 15  
 1 5 10  
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 30  
 20 25  
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 45  
 35 40  
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys 60  
 50 55  
 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser 80  
 65 70 75  
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 95  
 85 90  
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 110  
 100 105

20/102

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125  
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 130 135 140  
 aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 145 150 155 160  
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175  
 aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala  
 180 185 190  
 atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct 624  
 Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
 195 200 205  
 gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
 210 215 220  
 aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg 720  
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu  
 225 230 235 240  
 ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata 768  
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile  
 245 250 255  
 caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg 816  
 Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu  
 260 265 270  
 tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat 864  
 Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp  
 275 280 285  
 gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag 912  
 Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys  
 290 295 300  
 aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa 960  
 Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln  
 305 310 315 320  
 ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008  
 Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
 325 330 335  
 ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta 1056  
 Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
 340 345 350

0559716-051500

Sub A1

Sub A1

ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104  
 Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala  
 355 360 365

aat tca gtt aaa gag ctt ac  
 Asn Ser Val Lys Glu Leu  
 370

1124

<210> 26  
 <211> 373  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 26  
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
 1 5 10 15  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
 20 25 30  
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu  
 35 40 45  
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60  
 His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu  
 65 70 75 80  
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp  
 85 90 95  
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys  
 100 105 110  
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu  
 115 120 125  
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys  
 130 135 140  
 Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe  
 145 150 155 160  
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn  
 165 170 175  
 Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met  
 180 185 190  
 Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp  
 195 200 205  
 Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr  
 210 215 220  
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu  
 225 230 235 240  
 Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln  
 245 250 255  
 Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu  
 260 265 270  
 Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly  
 275 280 285  
 Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys  
 290 295 300  
 Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu  
 305 310 315 320

006750 067500

Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile  
 325 330 335  
 Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
 340 345 350  
 Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn  
 355 360 365  
 Ser Val Lys Glu Leu  
 370

<210> 27  
 <211> 1137  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<221> CDS  
 <222> (1)...(1137)

<400> 27  
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 1 5 10 15  
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
 20 25 30  
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45  
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
 50 55 60  
 ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
 65 70 75 80  
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
 85 90 95  
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
 100 105 110  
 aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125  
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 130 135 140

00595745-061900

Sub A1

23/102

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
 180 185 190

aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca 624  
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
 195 200 205

aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt 672  
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
 210 215 220

aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt 720  
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val  
 225 230 235 240

gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa 768  
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys  
 245 250 255

aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga 816  
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly  
 260 265 270

tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa 864  
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys  
 275 280 285

ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag 912  
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys  
 290 295 300

gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac 960  
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His  
 305 310 315 320

aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc 1008  
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala  
 325 330 335

att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa 1056  
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu  
 340 345 350

aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg 1104  
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met  
 355 360 365

ctt act aat tca gtt aaa gag ctt aca agc taa 1137  
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser \*  
 370 375

00595745-051900

Sub A1

SubA1  
 <210> 28  
 <211> 378  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 28  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 1 5 10 15  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
 20 25 30  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45  
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
 50 55 60  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
 65 70 75 80  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
 85 90 95  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
 100 105 110  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 130 135 140  
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Leu Gly Lys Leu  
 145 150 155 160  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
 180 185 190  
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
 195 200 205  
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
 210 215 220  
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val  
 225 230 235 240  
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys  
 245 250 255  
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly  
 260 265 270  
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys  
 275 280 285  
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys  
 290 295 300  
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His  
 305 310 315 320  
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala  
 325 330 335  
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu  
 340 345 350  
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met  
 355 360 365  
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 370 375

006510-9423560

Sub A1  
 <210> 29  
 <211> 1133  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<221> CDS  
 <222> (1)...(1133)

<400> 29  
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 1 5 10 15  
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
 20 25 30  
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 35 40 45  
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 50 55 60  
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 65 70 75 80  
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 85 90 95  
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 100 105 110  
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 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125  
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 130 135 140  
 aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 145 150 155 160  
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
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Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
50 55 60 65 70 75 80 85 90 95 100

50 55 60  
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
65 70 75 80  
Lys Glu Lys Leu

65                      70                      75  
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100 105 110  
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 115 120 125  
 Thr Ile Leu

Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu

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Ala Met Lys Ala

145 150 155 160  
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Lys	Pro	Ser	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala
			195				200					205			

Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser

210  
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 235 230 235 240

225 230 235 240  
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly  
245 250 255 260

Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn

Gly Thr Leu<sup>260</sup> Leu Ala Gly Ala Tyr<sup>265</sup> Thr Ile Ser Lys Leu<sup>270</sup> Ile Thr Gln  
275 280 285

Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu

Asn 285 Ala 290 Lys 295 Lys 300 Cys 305 Ser 310 Glu 315 Asp 320 Phe 325 Thr 330 Lys 335 Lys 340 Leu 345 Glu 350 Gly 355 Glu 360

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340 345 350

Ala Ile Leu 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 110

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 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45

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tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
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 100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
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 115 120 125

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 130 135 140

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 180 185 190

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Sub A1

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 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile  
 225 230 235 240  
 gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt 768  
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly  
 245 250 255  
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 260 265 270  
 gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa 864  
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 290 295 300  
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 Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu  
 305 310 315 320  
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 Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys  
 325 330 335  
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 340 345 350  
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30/102

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 115 120 125  
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 225 230 235 240  
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu  
 245 250 255  
 Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala  
 260 265 270  
 Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu  
 275 280 285  
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 290 295 300  
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 115 120 125  
 ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
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 130 135 140  
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 145 150 155 160  
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 165 170 175  
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 180 185 190  
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 Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
 195 200 205  
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 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
 210 215 220  
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 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile  
 225 230 235 240

Sub A1

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 260 265 270

tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca 864  
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 275 280 285

gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa 912  
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 290 295 300

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 305 310 315 320

gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat 1008  
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 325 330 335

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 340 345 350

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 35 40 45  
 Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys  
 50 55 60  
 Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu  
 65 70 75 80  
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 85 90 95

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Sub A1

Sub-A1

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Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys  
130 135 140  
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145 150 155 160  
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
165 170 175  
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180 185 190  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
195 200 205  
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210 215 220  
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
225 230 235 240  
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
245 250 255  
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
260 265 270  
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
275 280 285  
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
290 295 300  
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
305 310 315 320  
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
325 330 335  
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

34/102

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
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 35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
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 50 55 60

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 65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
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 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
 100 105 110

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 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
 115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
 130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
 145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
 165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
 180 185 190

tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt 624  
 Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val  
 195 200 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672  
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn  
 210 215 220

gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata 720  
 Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile  
 225 230 235 240

gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt 768  
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly  
 245 250 255

ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct 816  
 Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala  
 260 265 270

005745-051000

Sub-A1

Sub A1

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat	864
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn	
275 280 285	
tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa	912
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu	
290 295 300	
gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa	960
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu	
305 310 315 320	
aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca	1008
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala	
325 330 335	
gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta	1056
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val	
340 345 350	
gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa	1104
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys	
355 360 365	
gag ctt ac	1112
Glu Leu	
370	

<210> 36  
 <211> 369  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 36

Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala	
1 5 10 15	
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
20 25 30	
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu	
35 40 45	
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys	
50 55 60	
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu	
65 70 75 80	
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys	
85 90 95	
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys	
100 105 110	
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu	
115 120 125	
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys	
130 135 140	
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu	
145 150 155 160	

006746-061900

Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser  
 180 185 190  
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 195 200 205  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
 210 215 220  
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp  
 225 230 235 240  
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly  
 245 250 255  
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr  
 260 265 270  
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser  
 275 280 285  
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp  
 290 295 300  
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn  
 305 310 315 320  
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala  
 325 330 335  
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu  
 340 345 350  
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu  
 355 360 365  
 Leu

<210> 37  
 <211> 1106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<221> CDS  
 <222> (1)...(1106)

<400> 37  
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
 1 5 10 15  
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 35 40 45  
 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 50 55 60

0059546.061900

Sub A1

37/102

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu 80  
 65 70 75

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn 95  
 85 90

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln 110  
 100 105

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu 125  
 115 120

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys 140  
 130 135

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 160  
 145 150 155

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 175  
 165 170

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga 576  
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg 190  
 180 185

aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg 624  
 Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly 205  
 195 200

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672  
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val 220  
 210 215

gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa 720  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu 240  
 225 230 235

ctt gct acc aaa gct att ggt aag aaa ata gcc aat aat ggt tta gag 768  
 Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu 255  
 245 250

gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata 816  
 Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile 270  
 260 265

tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta 864  
 Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu 285  
 275 280

aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat 912  
 Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn 300  
 290 295

00596746-061900

Sub A1

aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat 960  
 Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp  
 305 310 315 320  
 gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag 1008  
 Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys  
 325 330 335  
 ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca 1056  
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser  
 340 345 350  
 aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt 1104  
 Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
 355 360 365  
 cc 1106

<210> 38  
 <211> 368  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 38  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
 1 5 10 15  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 35 40 45  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 50 55 60  
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
 65 70 75 80  
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
 85 90 95  
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
 100 105 110  
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
 115 120 125  
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
 130 135 140  
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
 145 150 155 160  
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
 165 170 175  
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg  
 180 185 190  
 Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly  
 195 200 205  
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
 210 215 220  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu  
 225 230 235 240

0055716-061000

Sub-A1

Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu  
 245 250 255  
 Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile  
 260 265 270  
 Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu  
 275 280 285  
 Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn  
 290 295 300  
 Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp  
 305 310 315 320  
 Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys  
 325 330 335  
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser  
 340 345 350  
 Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
 355 360 365

&lt;210&gt; 39

&lt;211&gt; 1107

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; OspC Chimera

&lt;221&gt; CDS

&lt;222&gt; (1)...(1107)

&lt;400&gt; 39

atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48  
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser  
 1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240  
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
 65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288  
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
 85 90 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336  
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
 100 105 110

00596745.061900

Sub A1

Sub A1  
 05595746 = 061900  
 tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384  
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
 115 120 125  
 ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432  
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
 130 135 140  
 aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
 145 150 155 160  
 aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
 165 170 175  
 gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg 576  
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
 180 185 190  
 aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg 624  
 Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
 195 200 205  
 cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672  
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
 210 215 220  
 gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag 720  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu  
 225 230 235 240  
 ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat 768  
 Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp  
 245 250 255  
 aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att 816  
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile  
 260 265 270  
 tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa 864  
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu  
 275 280 285  
 ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act 912  
 Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr  
 290 295 300  
 gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act 960  
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr  
 305 310 315 320  
 gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act 1008  
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr  
 325 330 335  
 aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg 1056  
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu  
 340 345 350

Sub A1  
 tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104  
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr  
 355 360 365

1107

agc  
 Ser

<210> 40  
 <211> 368  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 40  
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala 15  
 1 5 10  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 30  
 20 25  
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu 45  
 35 40  
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile 60  
 50 55 60  
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu 80  
 65 70 75  
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val 95  
 85 90  
 Leu Lys Asn Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys 110  
 100 105  
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly 125  
 115 120  
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys 140  
 130 135  
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys 160  
 145 150 155  
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala 175  
 165 170  
 Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys 190  
 180 185  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 205  
 195 200  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val 220  
 210 215  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu 240  
 225 230 235  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn 255  
 245 250  
 Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser 270  
 260 265  
 Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu 285  
 275 280  
 Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala 300  
 290 295  
 Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 320  
 305 310 315

09506746-061900

SubAI

Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys
				325					330					335	
Gly	Ala	Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser
			340					345					350		
Lys	Ala	Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser
		355					360					365			

<210> 41  
 <211> 1106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<221> CDS  
 <222> (1)...(1106)

<400> 41

atg	gct	tgt	aat	aat	tca	gga	aaa	gat	ggg	aat	gca	tct	gca	aat	tct	48
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser	
1				5					10					15		
gct	gat	gag	tct	ggt	aaa	ggg	ctt	aat	ctt	aca	gaa	ata	agt	aaa	aaa	96
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
			20					25					30			
att	aca	gaa	tct	aac	gca	ggt	ggt	ctg	gcc	gtg	aaa	gaa	ggt	gag	acc	144
Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	
			35				40					45				
tta	ctt	gca	tct	ata	gat	gaa	ctt	gct	acc	aaa	gct	att	ggt	aaa	aaa	192
Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	
		50				55			60							
ata	ggc	aat	aat	ggt	tta	gag	gcc	aat	cag	agt	aaa	aac	aca	tca	ttg	240
Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	
65					70				75						80	
tta	tca	gga	gct	tat	gca	ata	tct	gac	cta	ata	gca	gaa	aaa	tta	aat	288
Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	
				85				90						95		
gta	ttg	aaa	aat	gaa	gaa	tta	aag	gaa	aag	att	gat	aca	gct	aag	caa	336
Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	
			100					105					110			
tgt	tct	aca	gaa	ttt	act	aat	aaa	cta	aaa	agt	gaa	cat	gca	gtg	ctt	384
Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu	
			115				120					125				
ggt	ctg	gac	aat	ctt	act	gat	gat	aat	gca	caa	aga	gct	att	tta	aaa	432
Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	
						135					140					

0055746-051000

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480  
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
 145 150 155 160  
 aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528  
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
 165 170 175  
 gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga 576  
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly  
 180 185 190  
 aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg 624  
 Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
 195 200 205  
 cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672  
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
 210 215 220  
 gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa 720  
 Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu  
 225 230 235 240  
 ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta 768  
 Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu  
 245 250 255  
 gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca 816  
 Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr  
 260 265 270  
 ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa 864  
 Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu  
 275 280 285  
 aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt 912  
 Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe  
 290 295 300  
 act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt 960  
 Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val  
 305 310 315 320  
 act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa 1008  
 Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys  
 325 330 335  
 gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac 1056  
 Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn  
 340 345 350  
 ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt 1104  
 Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 355 360 365  
 ac 1106

Sub A1  
 <211> 367  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OspC Chimera

<400> 42  
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala  
 1 5 10 15  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile  
 20 25 30  
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu  
 35 40 45  
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile  
 50 55 60  
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu  
 65 70 75 80  
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val  
 85 90 95  
 Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys  
 100 105 110  
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly  
 115 120 125  
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys  
 130 135 140  
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys  
 145 150 155 160  
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala  
 165 170 175  
 Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys  
 180 185 190  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 195 200 205  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 210 215 220  
 Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 225 230 235 240  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala  
 245 250 255  
 Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile  
 260 265 270  
 Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys  
 275 280 285  
 Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr  
 290 295 300  
 Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr  
 305 310 315 320  
 Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp  
 325 330 335  
 Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu  
 340 345 350  
 Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 355 360 365

<210> 43  
 <211> 633  
 <212> DNA

&lt;213&gt; Borrelia burgdorferi

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)... (633)

&lt;400&gt; 43

atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48  
 Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
 1 5 10 15

ata tct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 96  
 Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 20 25 30

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 144  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
 35 40 45

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 192  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 50 55 60

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 240  
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
 65 70 75 80

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 288  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
 85 90 95

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 336  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
 100 105 110

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 384  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
 115 120 125

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 432  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 130 135 140

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 480  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 145 150 155 160

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 528  
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 165 170 175

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 576  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 180 185 190

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt coa aaa 624  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
 195 200 205

Sub A1

00596746-051900

aaa cct taa  
Lys Pro \*  
210

<210> 44  
<211> 209  
<212> PRT  
<213> Borrelia burgdorferi

<400> 44  
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile  
1 5 10 15  
Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
20 25 30  
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile  
35 40 45  
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu  
50 55 60  
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile  
65 70 75 80  
His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu  
85 90 95  
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp  
100 105 110  
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys  
115 120 125  
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu  
130 135 140  
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys  
145 150 155 160  
Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe  
165 170 175  
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn  
180 185 190  
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys  
195 200 205  
Pro

<210> 45  
<211> 580  
<212> DNA  
<213> Borrelia burgdorferi

<220>  
<221> CDS  
<222> (1)...(580)

<400> 45  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15  
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys  
20 25 30

00506746.061900

Sub-A1

47/102

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45  
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
 50 55 60  
 ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser  
 65 70 75 80  
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
 85 90 95  
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
 100 105 110  
 aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125  
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 130 135 140  
 aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 145 150 155 160  
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175  
 aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser  
 180 185 190  
 atg g 580  
 Met

<210> 46  
 <211> 192  
 <212> PRT  
 <213> Borrelia burgdorferi

<400> 46  
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala  
 1 5 10 15  
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile  
 20 25 30  
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu  
 35 40 45  
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60

00596745-061600

Sub A1

His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu  
 65 70 75 80  
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp  
 85 90 95  
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys  
 100 105 110  
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu  
 115 120 125  
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys  
 130 135 140  
 Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe  
 145 150 155 160  
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn  
 165 170 175  
 Ser Val Lys Glu Leu Thr Ser Pro Val Ala Glu Ser Pro Ser Met  
 180 185 190

<210> 47  
 <211> 639  
 <212> DNA  
 <213> Borrelia garinii

<220>  
 <221> CDS  
 <222> (1)...(639)

<400> 47  
 atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48  
 Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe  
 1 5 10 15  
 ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat 96  
 Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn  
 20 25 30  
 cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa 144  
 Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
 35 40 45  
 aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag 192  
 Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu  
 50 55 60  
 act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa 240  
 Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln  
 65 70 75 80  
 aaa ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga 288  
 Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly  
 85 90 95  
 tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa 336  
 Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys  
 100 105 110  
 ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag 384  
 Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys  
 115 120 125

005745-051900

Sub A1

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat 432  
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His  
 130 135 140  
 gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct 480  
 Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala  
 145 150 155 160  
 att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa 528  
 Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys  
 165 170 175  
 gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca 576  
 Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala  
 180 185 190  
 cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt 624  
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser  
 195 200 205  
 cca aaa aaa cct taa 639  
 Pro Lys Lys Pro \*  
 210

<210> 48  
 <211> 211  
 <212> PRT  
 <213> Borrelia garinii

<400> 48  
 Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile  
 1 5 10 15  
 Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro  
 20 25 30  
 Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 35 40 45  
 Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
 50 55 60  
 Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
 65 70 75 80  
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
 85 90 95  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
 100 105 110  
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
 115 120 125  
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
 130 135 140  
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
 145 150 155 160  
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
 165 170 175  
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
 180 185 190  
 Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro  
 195 200 205

005390-3425660

Sub A1

<220>  
<221> CDS  
<222> (1) . . . (624)

**SECRET**

51/102

cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576  
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val  
180 185 190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624  
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro \*  
195 200 205

<210> 50  
<211> 206  
<212> PRT  
<213> Borrelia afzelii

<400> 50  
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile  
1 5 10 15  
Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu  
20 25 30  
Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp  
35 40 45  
Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser  
50 55 60  
Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp  
65 70 75 80  
Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly  
85 90 95  
Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn  
100 105 110  
Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln  
115 120 125  
Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln  
130 135 140  
Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly  
145 150 155 160  
Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu  
165 170 175  
Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys  
180 185 190  
Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
195 200 205

<210> 51  
<211> 1680  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1680)

<400> 51  
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

00596746-05100

SubA1

**SECRET**

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa																	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys																	
202530																	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg																	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala																	
354045																	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa																	192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys																	
505560																	
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca																	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser																	
65707580																	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta																	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu																	
859095																	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag																	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys																	
100105110																	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat																	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp																	
115120125																	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta																	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu																	
130135140																	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta																	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu																	
145150155160																	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct																	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala																	
165170175																	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc																	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala																	
180185190																	
atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct																	624
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro																	
195200205																	
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa																	672
Ala Asp Glu Ser Ala Lys Gly Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys																	
210215220																	
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act																	720
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr																	
225230235240																	
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa																	768
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys																	
245250255																	

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 816  
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
 260 265 270

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 864  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
 275 280 285

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 912  
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
 290 295 300

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 960  
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
 305 310 315 320

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 1008  
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
 325 330 335

tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat 1056  
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
 340 345 350

tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta 1104  
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
 355 360 365

act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat 1152  
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp  
 370 375 380

tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc 1200  
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr  
 385 390 395 400

gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg 1248  
 Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val  
 405 410 415

aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct 1296  
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala  
 420 425 430

att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat 1344  
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn  
 435 440 445

cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata 1392  
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile  
 450 455 460

aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att 1440  
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile  
 465 470 475 480

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Sub A1

SubA1

aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat	1488
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp	
485 490 495	
agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa	1536
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys	
500 505 510	
aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa	1584
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu	
515 520 525	
ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa	1632
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln	
530 535 540	
gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca	1680
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala	
545 550 555 560	

<210> 52  
 <211> 560  
 <212> PRT  
 <213> ospC Chimera

<400> 52

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
210 215 220	
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
225 230 235 240	

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Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
 245 250 255  
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
 260 265 270  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
 275 280 285  
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
 290 295 300  
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
 305 310 315 320  
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
 325 330 335  
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
 340 345 350  
 Leu Phe Glu Ser Val Glu Gly Leu Lys Ala Ala Gln Val Ala Leu  
 355 360 365  
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp  
 370 375 380  
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr  
 385 390 395 400  
 Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val  
 405 410 415  
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala  
 420 425 430  
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn  
 435 440 445  
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile  
 450 455 460  
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile  
 465 470 475 480  
 Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp  
 485 490 495  
 Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys  
 500 505 510  
 Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu  
 515 520 525  
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 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192  
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
 65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
 100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
 115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
 130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
 145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
 165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
 180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624  
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
 195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672  
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
 210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720  
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
 225 230 235 240

ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat 768  
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
 245 250 255

005945-061900

Sub A1

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aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata 816  
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 260 265 270  
 tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta 864  
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
 275 280 285  
 aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act 912  
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
 290 295 300  
 aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat 960  
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
 305 310 315 320  
 gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag 1008  
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys  
 325 330 335  
 ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca 1056  
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser  
 340 345 350  
 aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat 1104  
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn  
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 cct gtt gtg gca gaa agt cca aaa aaa cct taa 1137  
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 370 375

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 <212> PRT  
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 20 25 30  
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 35 40 45  
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60  
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
 65 70 75 80  
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
 85 90 95  
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
 100 105 110  
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
 115 120 125  
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
 130 135 140  
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
 145 150 155 160

005120-049500

Sub A1

Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
 165 170 175  
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
 180 185 190  
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
 195 200 205  
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
 210 215 220  
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
 225 230 235 240  
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
 245 250 255  
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
 260 265 270  
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
 275 280 285  
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
 290 295 300  
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
 305 310 315 320  
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys  
 325 330 335  
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser  
 340 345 350  
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn  
 355 360 365  
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 370 375

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 1 5 10 15  
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 20 25 30  
 att acg gat tct aat gcg gtt tta ctt gct gtt aaa gag gtt gaa gcg 144  
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
 35 40 45  
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192  
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
 50 55 60  
 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
 65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288  
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu  
 85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336  
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys  
 100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384  
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp  
 115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432  
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu  
 130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480  
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu  
 145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528  
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala  
 165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576  
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys  
 180 185 190

aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat 624  
 Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn  
 195 200 205

cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa 672  
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys  
 210 215 220

att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct 720  
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala  
 225 230 235 240

ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata 768  
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile  
 245 250 255

aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg 816  
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
 260 265 270

ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt 864  
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser  
 275 280 285

gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat 912  
 Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp  
 290 295 300

Sub A1

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Sub A1

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Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu	
305 310 315 320	
ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa	1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys	
325 330 335	
aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt	1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe	
340 345 350	
aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat	1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn	
355 360 365	
tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa	1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys	
370 375 380	
cct taa	1158
Pro *	
385	

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20 25 30	
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu	
35 40 45	
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu	
65 70 75 80	
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp	
85 90 95	
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys	
100 105 110	
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu	
115 120 125	
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys	
130 135 140	
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe	
145 150 155 160	
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn	
165 170 175	
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys	
180 185 190	
Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile	
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006130-9436560

Sub A1

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1				5					10					15						
																		96		
gct	gac	gag	tct	gcg	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agc	aaa	aaa					
Ala	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys					
			20					25					30							
																		144		
att	aca	gat	tct	aat	gca	ttt	gta	ctt	gct	ggt	aaa	gaa	ggt	gag	act					
Ile	Thr	Asp	Ser	Asn	Ala	Phe	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr					
		35					40					45								
																		192		
ttg	ggt	tta	tct	ata	gat	gaa	ctt	gct	aag	aaa	gct	att	ggt	caa	aaa					
Leu	Val	Leu	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys					
	50					55					60									
																		240		
ata	gac	aat	aat	aat	ggt	tta	gct	gct	tta	aat	aat	cag	aat	gga	tcg					
Ile	Asp	Asn	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Asn	Asn	Gln	Asn	Gly	Ser					
65					70					75					80					
																		288		
ttg	tta	gca	gga	gcc	tat	gca	ata	tca	acc	cta	ata	aca	gaa	aaa	ttg					
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Thr	Glu	Lys	Leu					
				85					90					95						
																		336		
agt	aaa	ttg	aaa	aat	tta	gaa	gaa	tta	aag	aca	gaa	att	gca	aag	gct					
Ser	Lys	Leu	Lys	Asn	Leu	Glu	Glu	Leu	Lys	Thr	Glu	Ile	Ala	Lys	Ala					
			100					105					110							

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 384  
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 115 120 125  
 gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 432  
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile  
 130 135 140  
 tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat 480  
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
 145 150 155 160  
 tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta 528  
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
 165 170 175  
 act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca 576  
 Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro  
 180 185 190  
 aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act 624  
 Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
 195 200 205  
 aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 672  
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
 210 215 220  
 aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 720  
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
 225 230 235 240  
 gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 768  
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
 245 250 255  
 ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 816  
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
 260 265 270  
 ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 864  
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Thr Gln Lys Leu  
 275 280 285  
 agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 912  
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys  
 290 295 300  
 gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 960  
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
 305 310 315 320  
 ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1008  
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 305 310 315 320  
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 325 330 335  
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
 340 345 350  
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
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 370 375 380  
 Lys Pro  
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 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125

0055745 061900

SubA1

65/102

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
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 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat 672  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc 768  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245 250 255

gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct 816  
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala  
 260 265 270

aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag 864  
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu  
 275 280 285

gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac 912  
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn  
 290 295 300

tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag 960  
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys  
 305 310 315 320

gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa 1008  
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys  
 325 330 335

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056  
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
 340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
 355 360 365

Sub-A1

006790-061000

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152  
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197  
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390 395

<210> 60  
 <211> 398  
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 1 5 10 15  
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp  
 20 25 30  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala  
 65 70 75 80  
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr  
 85 90 95  
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys  
 115 120 125  
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys  
 130 135 140  
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala  
 145 150 155 160  
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly  
 165 170 175  
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys  
 180 185 190  
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
 195 200 205  
 Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly  
 210 215 220  
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu  
 225 230 235 240  
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala  
 245 250 255  
 Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys  
 260 265 270  
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala  
 275 280 285  
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu  
 290 295 300  
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala  
 305 310 315 320  
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu  
 325 330 335

0055745-051900

SubA1

Sub-A1

Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn  
 340 345 350  
 Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala  
 355 360 365  
 Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala  
 370 375 380  
 Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390 395

<210> 61  
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 <212> DNA  
 <213> ospC Chimera

<220>  
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 <222> (1)...(1196)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160

006745-05100

Sub A1

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat 672  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg 768  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245 250 255

gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct 816  
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 260 265 270

act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc 864  
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
 275 280 285

gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca 912  
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 290 295 300

aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta 960  
 Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
 305 310 315 320

aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa 1008  
 Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys  
 325 330 335

aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat 1056  
 Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp  
 340 345 350

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag 1104  
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys  
 355 360 365

ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca 1152  
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala  
 370 375 380

00596746-061900

Sub A1

00505745-051000

Sub A1

00505745-051000

Sub A1

00505745-051000

Sub A1

00505745-051000

Sub A1

00505745-051000

Sub-A1

Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ala	Lys
370						375					380				
Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu			
385					390					395					

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65 70 75 80	
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85 90 95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
 180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
 195 200 205

agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct 672  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
 210 215 220

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720  
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
 225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa 768  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
 245 250 255

gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt 816  
 Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly  
 260 265 270

aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac 864  
 Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn  
 275 280 285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa 912  
 Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys  
 290 295 300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa 960  
 Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu  
 305 310 315 320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa 1008  
 Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu  
 325 330 335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa 1056  
 His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys  
 340 345 350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt 1104  
 Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu  
 355 360 365

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gaa gct aaa gag 1152  
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu  
 370 375 380

atg ctt act aat tca gtt aaa gag ctt aca agc 1185  
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390 395

<211> 394  
 <212> PRT  
 <213> ospC Chimera

<400> 64  
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp  
 20 25 30  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala  
 65 70 75 80  
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu  
 85 90 95  
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr  
 100 105 110  
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys  
 115 120 125  
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys  
 130 135 140  
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu  
 145 150 155 160  
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys  
 165 170 175  
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
 210 215 220  
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
 225 230 235 240  
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val  
 245 250 255  
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys  
 260 265 270  
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly  
 275 280 285  
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys  
 290 295 300  
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys  
 305 310 315 320  
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His  
 325 330 335  
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala  
 340 345 350  
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu  
 355 360 365  
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met  
 370 375 380  
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390

<210> 65  
 <211> 1184

095945-061900

Sub-A1

<212> DNA  
<213> ospC Chimera

<220>  
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
195 200 205

00507950500

SubA1

Sub A1

<400> 66  
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala  
1 5 10 15

Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp  
 20 25 30  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala  
 65 70 75 80  
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu  
 85 90 95  
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr  
 100 105 110  
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys  
 115 120 125  
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys  
 130 135 140  
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu  
 145 150 155 160  
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys  
 165 170 175  
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala  
 210 215 220  
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
 225 230 235 240  
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile  
 245 250 255  
 Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly  
 260 265 270  
 Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn  
 275 280 285  
 Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln  
 290 295 300  
 Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu  
 305 310 315 320  
 Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu  
 325 330 335  
 His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys  
 340 345 350  
 Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu  
 355 360 365  
 Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu  
 370 375 380  
 Met Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

<210> 67  
 <211> 1184  
 <212> DNA  
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<220>  
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 <222> (1)...(1184)

005644-06100

Sub A1

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
 145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
 165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
 180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
 195 200 205

agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggc aat gca tct 672  
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
 210 215 220

00596746-061900

Sub A1

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~~<400> 68~~  
~~Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala~~  
~~1 5 10 15~~  
~~Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp~~  
~~20 25 30~~  
~~Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn~~  
~~35 40 45~~  
~~Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu~~  
~~50 55 60~~

78/102

Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala  
65 70 75 80  
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu  
85 90 95  
Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr  
100 105 110  
Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys  
115 120 125  
Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys  
130 135 140  
Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu  
145 150 155 160  
Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys  
165 170 175  
Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr  
210 215 220  
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser  
225 230 235 240  
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val  
245 250 255  
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly  
260 265 270  
Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr  
275 280 285  
Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys  
290 295 300  
Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala  
305 310 315 320  
Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala  
325 330 335  
Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile  
340 345 350  
Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys  
355 360 365  
Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu  
370 375 380  
Lys Asn Ala Val Lys Glu Leu Thr Ser  
385 390

<210> 69  
<211> 1209  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1209)

<400> 69  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

Sub A1

[illegible]

79/102													
ggt Gly 20	gct Ala	gag Glu	tca Ser	att Ile	gga Gly 25	tcc Ser	tgt Cys	aat Asn	aat Asn	tca Ser 30	ggg Gly	aa Lys	
aca Thr	tct Ser	gca Ala	aat Asn	tct Ser 40	gct Ala	gat Asp	gag Glu	tct Ser	ggt Val 45	aaa Lys	ggg Gly	cc Pro	
gaa Glu	ata Ile	agt Ser	aaa Lys 55	aaa Lys	att Ile	acg Thr	gat Asp	tct Ser 60	aat Asn	gcg Ala	ggt Val	tt Leu	
aaa Lys	gag Glu	ggt Val 70	gaa Glu	gcg Ala	ttg Leu	ctg Leu	tca Ser 75	tct Ser	ata Ile	gat Asp	gag Glu	ct Leu 8	
att Ile 85	ggt Gly	aaa Lys	aaa Lys	ata Ile	aaa Lys	aac Asn 90	gat Asp	ggt Gly	agt Ser	tta Leu	gat Asp 95	aa Asn	
cgc Arg 100	aac Asn	gag Glu	tca Ser	ttg Leu	tta Leu 105	gca Ala	gga Gly	gct Ala	tat Tyr	aca Thr 110	ata Ile	tc Ser	
aca Thr	caa Gln	aaa Lys	tta Leu	agt Ser 120	aaa Lys	tta Leu	aac Asn	gga Gly	tca Ser 125	gaa Glu	ggt Gly	tt Leu	
att Ile	gcc Ala	gca Ala	gct Ala 135	aag Lys	aaa Lys	tgc Cys	tct Ser	gaa Glu 140	gag Glu	ttt Phe	agt Ser	ac Thr	
gat Asp	aat Asn	cat His 150	gca Ala	cag Gln	ctt Leu	ggt Gly	ata Ile 155	cag Gln	ggc Gly	ggt Val	act Thr	ga Asn 16	
aaa Lys 165	aaa Lys	gct Ala	att Ile	tta Leu	aaa Lys	gca Ala 170	aat Asn	gca Ala	gcg Ala	ggt Gly	aaa Lys 175	ga Asn	
gaa Glu 180	gaa Glu	ctt Leu	gaa Glu	aag Lys	ttg Leu 185	tcc Ser	gga Gly	tca Ser	tta Leu	gaa Glu 190	agc Ser	tt Leu	
gct Ala	aaa Lys	gag Glu	atg Met 200	ctt Leu	gct Ala	aat Asn	tca Ser	ggt Val 205	aaa Lys	gag Glu	ctt Leu	ac Thr	
gtc Val	cat His	ggt Gly	aat Asn 215	aat Asn	tca Ser	ggt Gly	ggg Gly	gat Asp 220	tct Ser	gca Ala	tct Ser	ac Thr	
gag Glu	tct Ser	gca Ala	aaa Lys 230	gga Gly	cct Pro	aat Asn	ctt Leu 235	acc Thr	gta Val	ata Ile	agc Ser	aa Lys 24	
gat Asp 245	tct Ser	aat Asn	gca Ala	ttt Phe	tta Leu 250	ctg Leu	gct Ala	gtg Val	aaa Lys	gaa Glu	ggt Val 255	ga Glu	

Sub A1

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 816  
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
 260 265 270

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 864  
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
 275 280 285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 912  
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
 290 295 300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 960  
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys  
 305 310 315 320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 1008  
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
 325 330 335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1056  
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
 340 345 350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1104  
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
 355 360 365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1152  
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
 370 375 380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1200  
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
 385 390 395 400

aaa cct taa 1209  
 Lys Pro \*

<210> 70  
 <211> 401  
 <212> PRT  
 <213> ospC Chimera

<400> 70  
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala  
 1 5 10 15  
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp  
 20 25 30  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala  
 65 70 75 80

00614094256560

Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu  
 85 90 95  
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr  
 100 105 110  
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys  
 115 120 125  
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys  
 130 135 140  
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu  
 145 150 155 160  
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys  
 165 170 175  
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn  
 210 215 220  
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys  
 225 230 235 240  
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala  
 245 250 255  
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile  
 260 265 270  
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
 275 280 285  
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser  
 290 295 300  
 Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp  
 305 310 315 320  
 Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu  
 325 330 335  
 Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys  
 340 345 350  
 Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe  
 355 360 365  
 Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn  
 370 375 380  
 Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys  
 385 390 395 400  
 Pro

<210> 71  
 <211> 1179  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1179)

<400> 71  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115 120 125

gaa aag att gat aca gct aag caa tct tct aca gaa ttt act aat aaa 432  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
 180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
 195 200 205

att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat 672  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
 210 215 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
 225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gaa 768  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
 245 250 255

006130-043550

Sub A1

act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa 816  
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
 260 265 270  
 ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca 864  
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
 275 280 285  
 tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata 912  
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
 290 295 300  
 agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct 960  
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
 305 310 315 320  
 aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca 1008  
 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
 325 330 335  
 gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056  
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
 340 345 350  
 tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104  
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
 355 360 365  
 tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152  
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
 370 375 380  
 act aat tca gtt aaa gag ctt aca agc 1179  
 Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390

<210> 72  
 <211> 392  
 <212> PRT  
 <213> ospC Chimera

<400> 72  
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala  
 1 5 10 15  
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp  
 20 25 30  
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 65 70 75 80  
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn  
 85 90 95  
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp  
 100 105 110

00013054236560

Sub-A1

Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu  
 115 120 125  
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu  
 130 135 140  
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn  
 145 150 155 160  
 Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala  
 165 170 175  
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala  
 180 185 190  
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile  
 195 200 205  
 Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 210 215 220  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 225 230 235 240  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 245 250 255  
 Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
 260 265 270  
 Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu  
 275 280 285  
 Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser  
 290 295 300  
 Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys  
 305 310 315 320  
 Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp  
 325 330 335  
 Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu  
 340 345 350  
 Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu  
 355 360 365  
 Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr  
 370 375 380  
 Asn Ser Val Lys Glu Leu Thr Ser  
 385 390

<210> 73  
 <211> 1178  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1178)

<400> 73  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
 180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
 195 200 205

att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat 672  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
 210 215 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
 225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa 768  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
 245 250 255

act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa 816  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
 260 265 270

00596745-051900

Sub A1

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SubA1

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly	
275 280 285	
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys	
290 295 300	
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn	
305 310 315 320	
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His	
325 330 335	
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala	
340 345 350	
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met	
370 375 380	
ctt gct aat tca gtt aaa gag ctt ac	1178
Leu Ala Asn Ser Val Lys Glu Leu	
385 390	

<210> 74  
 <211> 391  
 <212> PRT  
 <213> ospC Chimera

<400> 74

Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala	
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Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp	
20 25 30	
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
50 55 60	
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
65 70 75 80	
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn	
85 90 95	
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp	
100 105 110	
Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu	
115 120 125	
Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu	
130 135 140	
Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn	
145 150 155 160	

05595746-051900

Sub A1

Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala  
 165 170 175  
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala  
 180 185 190  
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile  
 195 200 205  
 Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
 210 215 220  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 225 230 235 240  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr  
 245 250 255  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 260 265 270  
 Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr  
 275 280 285  
 Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu  
 290 295 300  
 Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala  
 305 310 315 320  
 Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala  
 325 330 335  
 Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile  
 340 345 350  
 Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys  
 355 360 365  
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 370 375 380  
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 385 390

<210> 75  
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<220>  
 <221> CDS  
 <222> (1)...(1178)

<400> 75  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60

**UNITED STATES DEPARTMENT OF AGRICULTURE**

ctg Leu 65	gcc Ala	gtg Val	aaa Lys	gaa Glu	gtt Val 70	gag Glu	acc Thr	tta Leu	ctt Leu	gca Ala 75	tct Ser	ata Ile	gat Asp	gaa Glu	ctt Leu 80	240
gct Ala	acc Thr	aaa Lys	gct Ala	att Ile 85	ggg Gly	aaa Lys	aaa Lys	ata Ile	ggc Gly 90	aat Asn	aat Asn	ggt Gly	tta Leu	gag Glu 95	gcc Ala	288
aat Asn	cag Gln	agt Ser	aaa Lys 100	aac Asn	aca Thr	tca Ser	ttg Leu	tta Leu 105	tca Ser	gga Gly	gct Ala	tat Tyr	gca Ala 110	ata Ile	tct Ser	336
gac Asp	cta Leu	ata Ile 115	gca Ala	gaa Glu	aaa Lys	tta Leu	aat Asn 120	gta Val	ttg Leu	aaa Lys	aat Asn 125	gaa Glu 130	gaa Glu	tta Leu	aag Lys	384
gaa Glu	aag Lys 130	att Ile	gat Asp	aca Thr	gct Ala	aag Lys 135	caa Gln	tgt Cys	tct Ser	aca Thr	gaa Glu 140	ttt Phe	act Thr	aat Asn	aaa Lys	432
cta Leu 145	aaa Lys	agt Ser	gaa Glu	cat His	gca Ala 150	gtg Val	ctt Leu	ggg Gly	ctg Leu	gac Asp 155	aat Asn	ctt Leu	act Thr	gat Asp 160	gat Asp	480
aat Asn	gca Ala	caa Gln	aga Arg	gct Ala 165	att Ile	tta Leu	aaa Lys	aaa Lys 170	cat His	gca Ala	aat Asn	aaa Lys	gat Asp	aag Lys 175	ggg Gly	528
gct Ala	gca Ala	gaa Glu	ctt Leu 180	gaa Glu	aag Lys	tta Leu	ttt Phe	aaa Lys 185	gag Ala	gta Val	gaa Glu	aac Asn	tta Leu 190	tca Ser	aaa Lys	576
gca Ala	gct Ala	caa Gln 195	gac Asp	aca Thr	tta Leu	aaa Lys	aat Asn 200	gct Ala	gtt Val	aaa Lys	gag Glu	ctt Leu 205	aca Thr	agt Ser	cct Pro	624
att Ile 210	gtc Val	cat His	ggg Gly	aat Asn	aat Asn	tca Ser 215	aga Arg	aaa Lys	gat Asp	ggg Gly 220	aat Asn	gca Ala	tct Ser	aca Thr	aat Asn	672
tct Ser 225	gcc Ala	gat Asp	gag Glu	tct Ser	gtt Val 230	aaa Lys	ggg Gly	cct Pro	aat Asn	ctt Leu 235	aca Thr	gaa Glu	ata Ile	agt Ser	aaa Lys 240	720
aaa Lys	att Ile	aca Thr	gaa Glu	tct Ser 245	aac Asn	gca Ala	gtt Val	gtt Val	ctg Leu 250	gcc Ala	gtg Val	aaa Lys	gaa Glu	gtt Val 255	gag Glu	768
acc Thr	tta Leu	ctt Leu	gca Ala 260	tct Ser	ata Ile	gat Asp	gaa Glu	ctt Leu 265	gct Ala	acc Thr	aaa Lys	gct Ala 270	att Ile	ggg Gly	aag Lys	816
aaa Lys	ata Ile	ggc Gly 275	aat Asn	aat Asn	ggg Gly	tta Leu	gag Glu 280	gcc Ala	aat Asn	cag Gln	agt Ser	aaa Lys 285	aac Asn	aca Thr	tca Ser	864
ttg Leu 290	tta Leu	tca Ser	gga Gly	gct Ala	tat Tyr	gca Ala 295	ata Ile	tct Ser	gac Asp	cta Leu	ata Ile 300	gca Ala	gaa Glu	aaa Lys	tta Leu	912

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960  
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys  
 305 310 315 320  
 caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008  
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val  
 325 330 335  
 ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056  
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu  
 340 345 350  
 aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104  
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
 355 360 365  
 ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152  
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys  
 370 375 380  
 aat gct gtt aaa gag ctt aca agt cc 1178  
 Asn Ala Val Lys Glu Leu Thr Ser  
 385 390

<210> 76  
 <211> 391  
 <212> PRT  
 <213> ospC Chimera

<400> 76  
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 20 25 30  
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 65 70 75 80  
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn  
 85 90 95  
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp  
 100 105 110  
 Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu  
 115 120 125  
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu  
 130 135 140  
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn  
 145 150 155 160  
 Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala  
 165 170 175  
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala  
 180 185 190  
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile  
 195 200 205

005054061900

Sub A1

Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser  
 210 215 220  
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
 225 230 235 240  
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr  
 245 250 255  
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys  
 260 265 270  
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu  
 275 280 285  
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn  
 290 295 300  
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln  
 305 310 315 320  
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu  
 325 330 335  
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys  
 340 345 350  
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe  
 355 360 365  
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn  
 370 375 380  
 Ala Val Lys Glu Leu Thr Ser  
 385 390

<210> 77  
 <211> 1230  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1230)

<400> 77  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95

005730-4736563

Sub-A1

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160

gct gat gca aaa gaa gac att tta aaa aca aat ggt act aaa act aaa 528  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca 672  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser  
 210 215 220

ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct 720  
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro  
 225 230 235 240

aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta 768  
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu  
 245 250 255

ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt 816  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 260 265 270

tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac 864  
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn  
 275 280 285

gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca 912  
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser  
 290 295 300

aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag 960  
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys  
 305 310 315 320

005506746-051900

92/102

aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008  
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys 335  
 325  
 cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056  
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp 350  
 340  
 aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly 365  
 355  
 gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152  
 Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys 380  
 370  
 gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200  
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro 400  
 385 390 395  
 gtt gtg gca gaa agt cca aaa aaa cct taa 1230  
 Val Val Ala Glu Ser Pro Lys Lys Pro \*  
 405

<210> 78  
 <211> 408  
 <212> PRT  
 <213> ospC Chimera

<400> 78  
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp  
 20 25 30  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala  
 65 70 75 80  
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr  
 85 90 95  
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys  
 115 120 125  
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys  
 130 135 140  
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala  
 145 150 155 160  
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly  
 165 170 175  
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys  
 180 185 190  
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
 195 200 205  
 Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser Gly  
 210 215 220

Sub A1

006799-06100

Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn  
 225 230 235 240  
 Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu  
 245 250 255  
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser  
 260 265 270  
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu  
 275 280 285  
 Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys  
 290 295 300  
 Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys  
 305 310 315 320  
 Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu  
 325 330 335  
 Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn  
 340 345 350  
 Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala  
 355 360 365  
 Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala  
 370 375 380  
 Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val  
 385 390 395 400  
 Val Ala Glu Ser Pro Lys Lys Pro  
 405

<210> 79  
 <211> 1209  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
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 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
 210 215 220

ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720  
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225 230 235 240

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
 245 250 255

gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat 816  
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
 260 265 270

gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta 864  
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
 275 280 285

gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta 912  
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
 290 295 300

att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga 960  
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
 305 310 315 320

gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt 1008

00505745051000

Sub-A1

95/102

Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
 325 330 335  
 act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt 1056  
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
 340 345 350  
 act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa 1104  
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
 355 360 365  
 act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152  
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
 370 375 380  
 ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200  
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 385 390 395 400  
 aca agc taa 1209  
 Thr Ser \*

<210> 80  
 <211> 401  
 <212> PRT  
 <213> ospC Chimera

<400> 80  
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp  
 20 25 30  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 35 40 45  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu  
 50 55 60  
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala  
 65 70 75 80  
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr  
 85 90 95  
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys  
 115 120 125  
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys  
 130 135 140  
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala  
 145 150 155 160  
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly  
 165 170 175  
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys  
 180 185 190  
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro  
 195 200 205  
 Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly  
 210 215 220

00596746-054600

Sub A1

SubA1

Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly  
 225 230 235 240  
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val  
 245 250 255  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu  
 260 265 270  
 Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp  
 275 280 285  
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile  
 290 295 300  
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu  
 305 310 315 320  
 Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr  
 325 330 335  
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr  
 340 345 350  
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr  
 355 360 365  
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu  
 370 375 380  
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr  
 385 390 395 400  
 Ser

<210> 81  
 <211> 1205  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1205)

<400> 81  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95

acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gcg	gga	gct	tat	gca	ata	336
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	
			100							105				110		
tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta	384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	
			115							120				125		
aag	gaa	aaa	att	gat	gcg	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat	432
Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	
			130							135				140		
aaa	tta	aaa	gaa	aaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggt	gtt	act	gat	480
Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	
			145							150				155		
gct	gat	gca	aaa	gaa	gcc	att	tta	aaa	aca	aat	ggt	act	aaa	act	aaa	528
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys	
			165							170				175		
ggt	gct	gaa	gaa	ctt	gga	aaa	tta	ttt	gaa	tca	gta	gag	gtc	ttg	tca	576
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	
			180							185				190		
aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	gtt	aaa	gag	ctt	aca	agc	624
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	
			195							200				205		
cct	gtt	gtg	gca	gaa	agt	cca	aaa	aaa	cct	tcc	atg	gta	aat	aat	tca	672
Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	Ser	Met	Val	Asn	Asn	Ser	
			210							215				220		
gga	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	720
Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	
			225							230				235		
ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	768
Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	
			245							250				255		
gtt	gtt	ctg	gct	gtg	aaa	gaa	att	gaa	act	ttg	ctt	gca	tct	ata	gat	816
Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	
			260							265				270		
gaa	ctt	gct	act	aaa	gct	att	ggt	aaa	aaa	ata	caa	caa	aat	ggt	ggt	864
Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	
			275							280				285		
tta	gct	gtc	gaa	gcg	ggg	cat	aat	gga	aca	ttg	tta	gca	ggt	gct	tat	912
Leu	Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	
			290							295				300		
aca	ata	tca	aaa	cta	ata	aca	caa	aaa	tta	gat	gga	ttg	aaa	aat	tca	960
Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	
			305							310				315		
															320	

98/102

Sub A1

gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp	
325 330 335	
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn	
340 345 350	
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct	1104
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala	
355 360 365	
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa	1152
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu	
370 375 380	
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag	1200
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu	
385 390 395 400	
ctt ac	1205
Leu	

<210> 82  
 <211> 400  
 <212> PRT  
 <213> ospC Chimera

<400> 82

Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala	
1 5 10 15	
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp	
20 25 30	
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu	
50 55 60	
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala	
65 70 75 80	
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr	
85 90 95	
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser	
100 105 110	
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys	
115 120 125	
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys	
130 135 140	
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala	
145 150 155 160	
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly	
165 170 175	
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys	
180 185 190	
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro	
195 200 205	
Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly	
210 215 220	

006799-05100

Sub A1

Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly
225					230				235						240
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val
			245						250					255	
Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu
			260					265					270		
Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu
		275				280						285			
Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr
	290					295					300				
Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu
305				310					315						320
Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe
			325						330					335	
Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val
			340					345					350		
Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys
		355					360					365			
Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn
	370					375					380				
Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu
385					390					395					400

<210> 83  
 <211> 1236  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1236)

<400> 83

atg	aga	tta	tta	ata	gga	ttt	gct	tta	gcg	tta	gct	tta	ata	gga	tgt	48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys	
1				5					10					15		
gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	agt	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Ser	Asn	Ser	Gly	Lys	
			20					25					30			
ggt	ggg	gat	tct	gca	tct	act	aat	cct	gct	gac	gag	tct	gcg	aaa	ggg	144
Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Ala	Asp	Glu	Ser	Ala	Lys	Gly	
		35					40					45				
cct	aat	ctt	aca	gaa	ata	agc	aaa	aaa	att	aca	gat	tct	aat	gca	ttt	192
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	
	50					55					60					
gta	ctt	gct	gtt	aaa	gaa	gtt	gag	act	ttg	gtt	tta	tct	ata	gat	gaa	240
Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Val	Leu	Ser	Ile	Asp	Glu	
	65				70					75					80	
ctt	gct	aag	aaa	gct	att	ggt	caa	aaa	ata	gac	aat	aat	aat	ggt	tta	288
Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys	Ile	Asp	Asn	Asn	Asn	Gly	Leu	
				85					90					95		

100/102

gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca 336  
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala  
100 105 110

ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa 384  
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu  
115 120 125

gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt 432  
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe  
130 135 140

act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct 480  
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala  
145 150 155 160

acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc 528  
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr  
165 170 175

gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt 576  
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly  
180 185 190

ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt 624  
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu  
195 200 205

aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat 672  
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn  
210 215 220

aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa 720  
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys  
225 230 235 240

gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca 768  
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala  
245 250 255

ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat 816  
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp  
260 265 270

gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta 864  
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu  
275 280 285

gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa 912  
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu  
290 295 300

ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa 960  
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu  
305 310 315 320

tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act 1008  
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr  
325 330 335

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Sub A1

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056  
 Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln  
 340 345 350

gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104  
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp  
 355 360 365

aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152  
 Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu  
 370 375 380

tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200  
 Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr  
 385 390 395 400

aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236  
 Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro \*

<210> 84  
 <211> 410  
 <212> PRT  
 <213> ospC Chimera

<400> 84  
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala  
 1 5 10 15  
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys Gly  
 20 25 30  
 Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Val  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Gly Leu Ala  
 85 90 95  
 Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu Glu  
 115 120 125  
 Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr  
 130 135 140  
 Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala Thr  
 145 150 155 160  
 Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr Asp  
 165 170 175  
 Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly Leu  
 180 185 190  
 Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu Thr  
 195 200 205  
 Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn Asn  
 210 215 220  
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
 225 230 235 240

05596745-051900

Sub A1

Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
 245 250 255  
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
 260 265 270  
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
 275 280 285  
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
 290 295 300  
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
 305 310 315 320  
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
 325 330 335  
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
 340 345 350  
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys  
 355 360 365  
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser  
 370 375 380  
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn  
 385 390 395 400  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
 405 410

00505745-051000

Sub A1